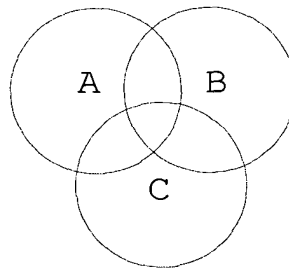


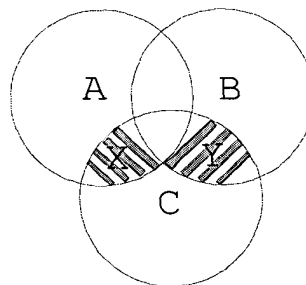
Reference sequence:  
Possible sub-sequences:

AGCTCATTGA  
AGCTCATTG  
GCTCATTGA  
AGCTCATT  
GCTCATTG  
CTCATTGA

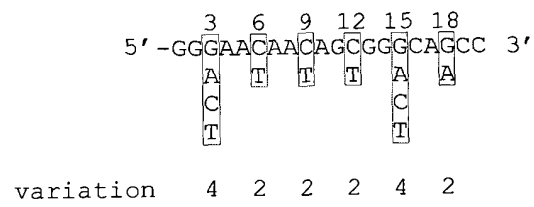
**FIGURE 1**



**FIGURE 2A**



**FIGURE 2B**



**FIGURE 3**

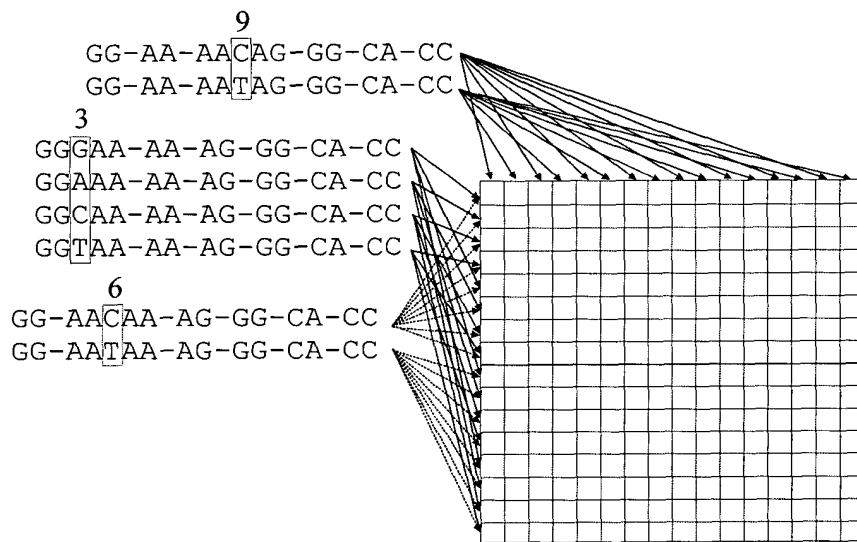
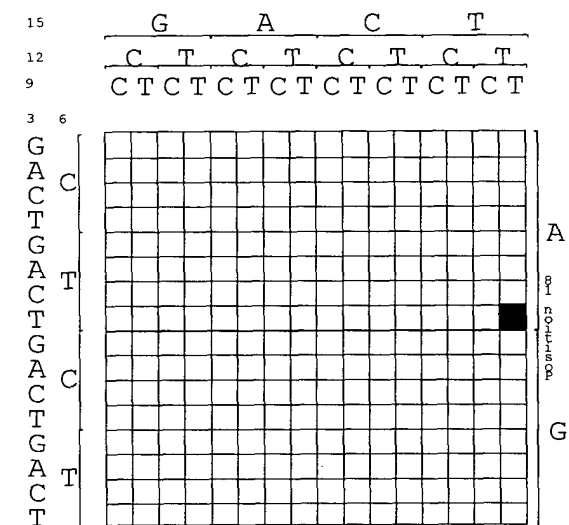
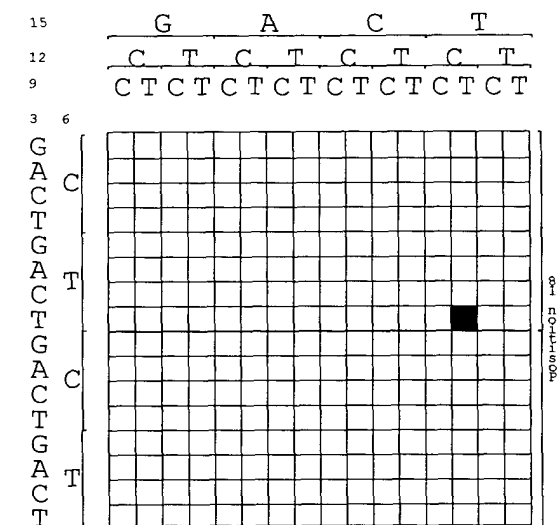


FIGURE 4

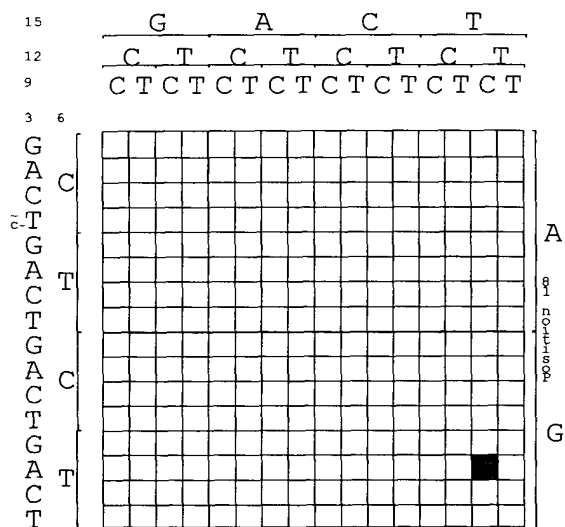
### Positions



### Positions



### Positions



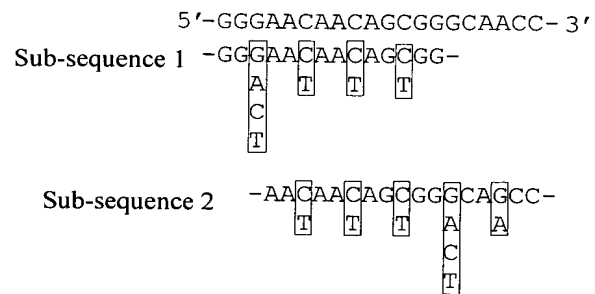
**FIGURE 6A****FIGURE 6B**

FIGURE 6C



FIGURE 6D







PVY-N PVY-NFR PVY-PA

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48
49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96
97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112
113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128
129	130	131	132	133	134	135	136								

PVY-Co

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48
49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96
97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112
113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128
129	130	131	132	133	134	135	136								

PVY-HUNG

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48
49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96
97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112
113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128
129	130	131	132	133	134	135	136								

BYMV-S

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48
49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96
97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112
113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128
129	130	131	132	133	134	135	136								

PVY-NSW

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48
49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96
97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112
113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128
129	130	131	132	133	134	135	136								

FIGURE 8

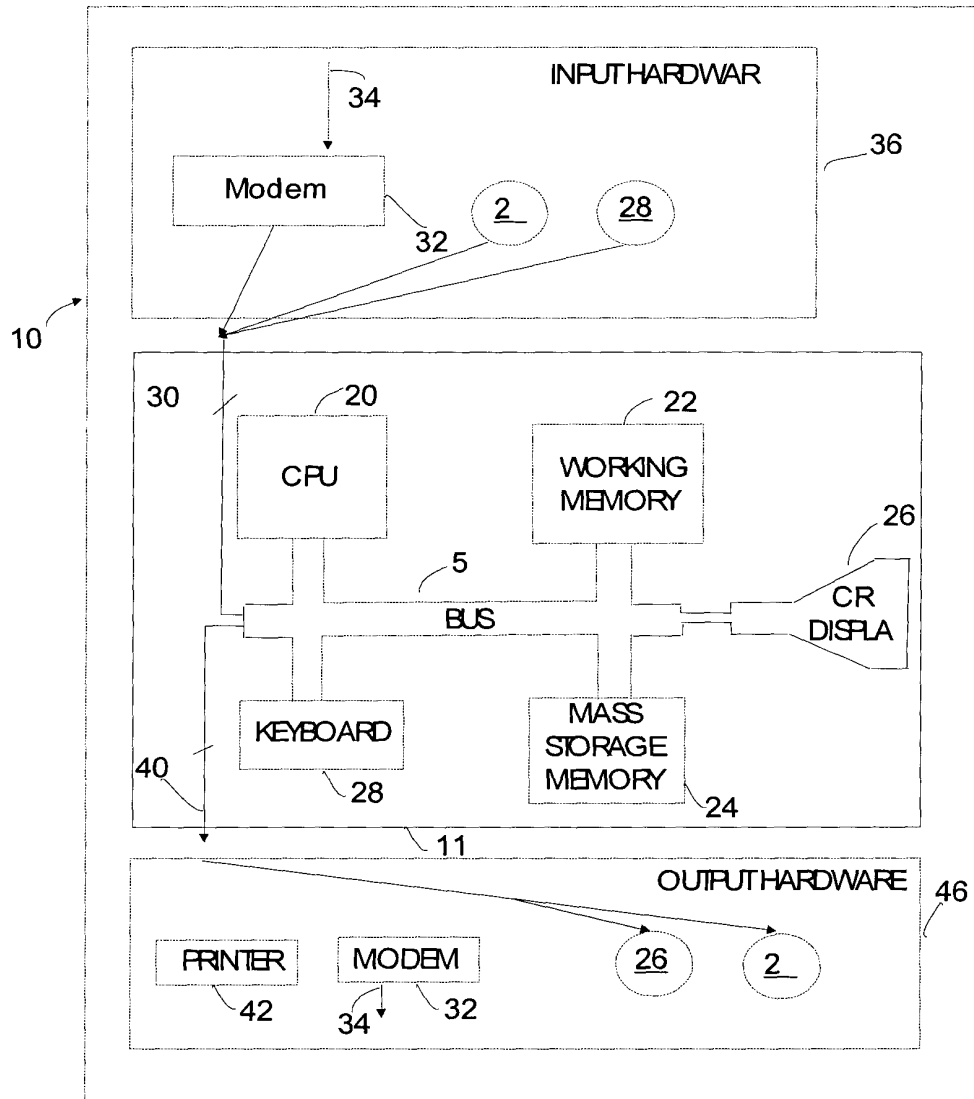
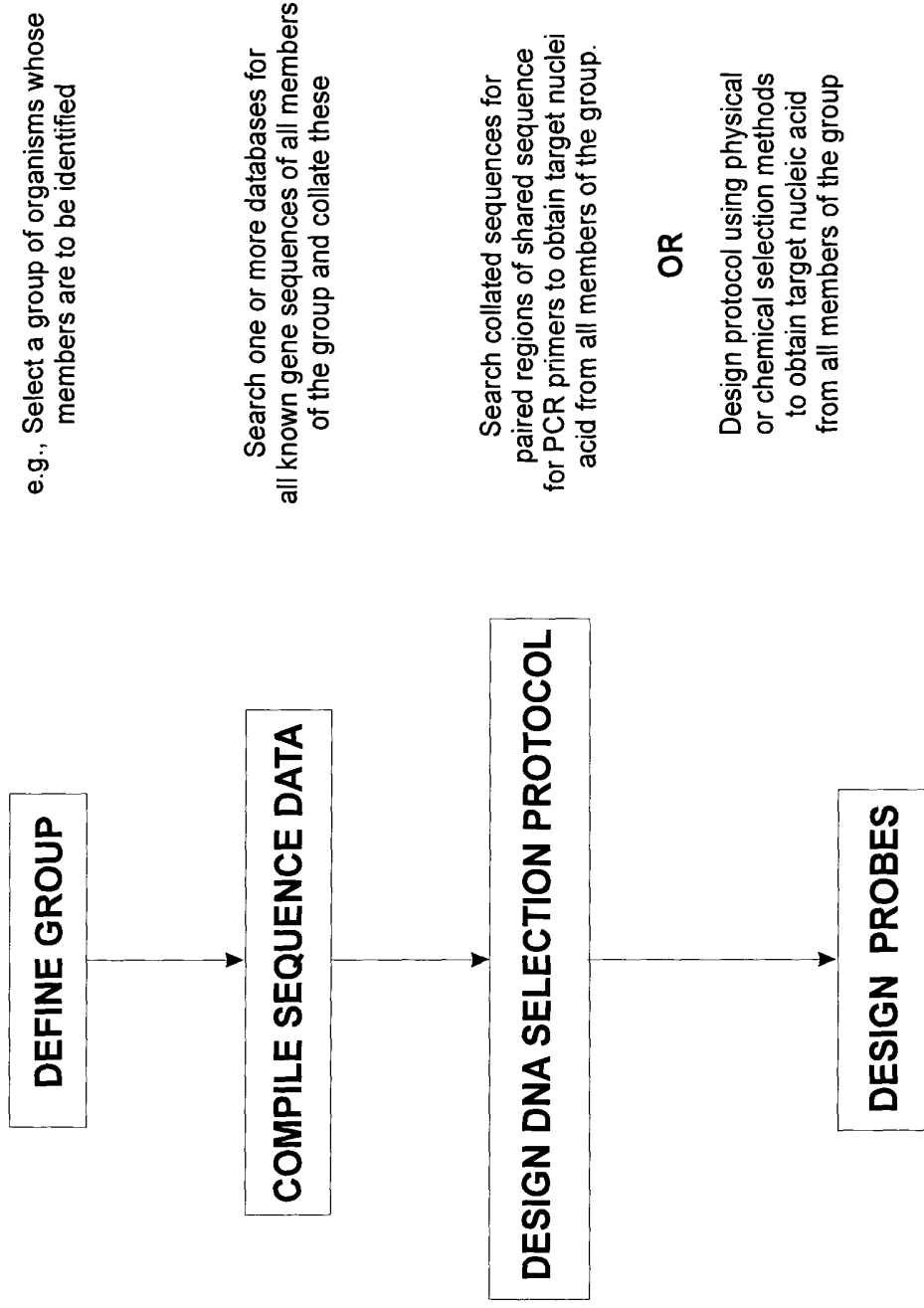
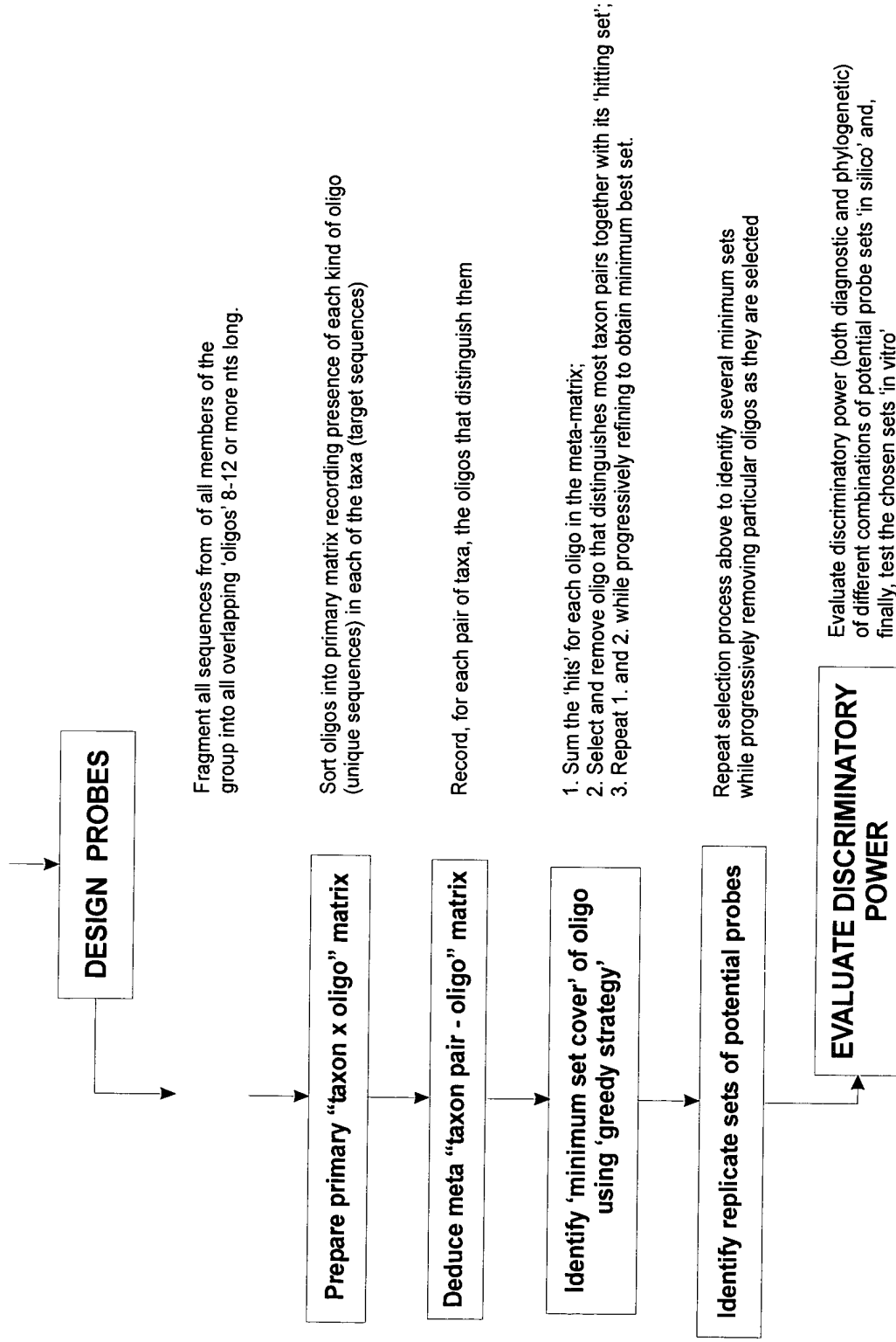


FIGURE 9



**FIGURE 10**

1. Fragment all sequences from of all members of the group into all overlapping 'oligos' 8-12 or more nts long.  
 2. Sort oligos into primary matrix recording presence of each kind of oligo (unique sequences) in each of the taxa (target sequences)  
 3. Record, for each pair of taxa, the oligos that distinguish them  
 4. 1. Sum the 'hits' for each oligo in the meta-matrix;  
 5. 2. Select and remove oligo that distinguishes most taxon pairs together with its 'hitting set';  
 6. 3. Repeat 1. and 2. while progressively refining to obtain minimum best set.  
 7. Repeat selection process above to identify several minimum sets while progressively removing particular oligos as they are selected  
 8. Evaluate discriminatory power (both diagnostic and phylogenetic) of different combinations of potential probe sets 'in silico' and, finally, test the chosen sets 'in vitro'



**FIGURE 10 contd.**

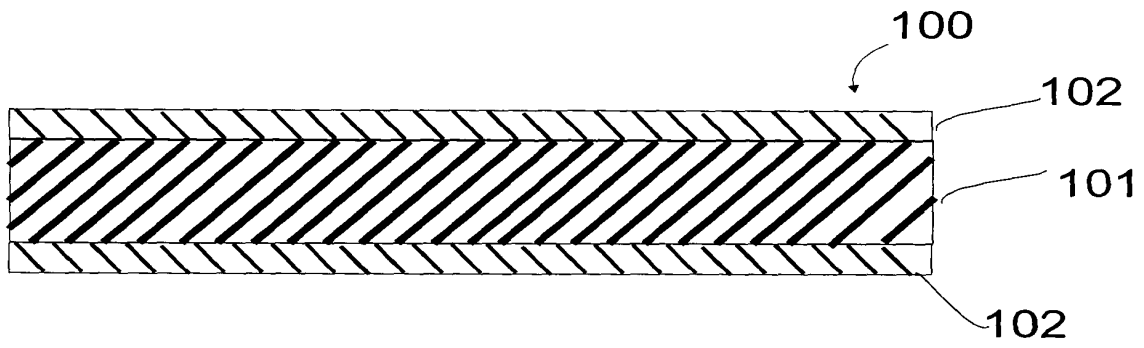


FIGURE 11

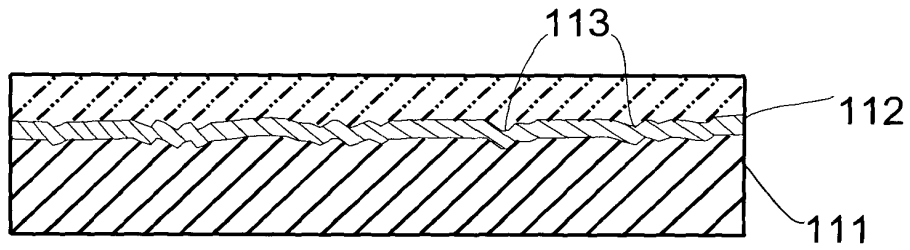


FIGURE 12